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SEQUENCE LISTING

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<120> Chimeric Polypeptides Allowing Expression of
Plant-Noxious Proteins

<130> 020829-000100US

<140> US 09/743,690

<141> 2001-01-12

<150> NZ 331002

<151> 1998-07-15

<150> WO PCT/NZ99/00110

<151> 1999-07-15

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:potato
proteinase inhibitor I (PPI-I/pUC19)

<220>

<221> CDS

<222> (1)..(324)

<223> PPI-I/pUC19

<400> 1

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ctcttggcac gaaaagaaag tgatggacca gagatccttag aacttcaaaa ggaatttgaa 120
tgcaatggaa aacaaagggt gccagaactt attggtgtac caacaaagct tgctaagggg 180
ataattgaga aggaaaattc actcataact aatgttcaga tactactgaa tggttctcca 240
gtcacaaatgg attatcggtt taatcgagtt cgtctttttg ataacatttt gggatgatgtt 300
gtacaaattc ctagggtggc ttaa                                     324
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<210> 2

<211> 576

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:avidin cDNA
 (pGEMav)

<220>
 <221> CDS
 <222> (44)..(502)
 <223> avidin (pGEMav)

<220>
 <221> sig_peptide
 <222> (44)..(115)
 <223> signal sequence

<400> 2
 gaattccgca aggagcacac ccggctgtcc acctgctgca gagatgggtgc acgcaacctc 60
 cccgctgctg ctgctgctgc tgctcagcct ggctctgggtg gctcccggga tccctgccag 120
 aaagtgtctg ctgactggga aatggaccaa cgatctgggc tccaacatga ccatcggggc 180
 tgtgaacagc agaggtgaat tcacaggcac ctacatcaca gccgtaacag ccacatcaaa 240
 tgagatcaaa gagtcaccac tgcattgggac acaaaacacc atcaacaaga ggaccagcc 300
 cacctttggc ttcaccgtca attggaagtt ttcagagtcc accactgtct tcacggggcca 360
 gtgcttcata gacaggaatg ggaaggaggt cctgaagacc atgtgggtgc tgcgggtcaag 420
 tgttaatgac attggtgatg actggaaaagc taccaggggc ggcatcaaca tcttcactcg 480
 cctgcgcaca cagaaggagt gaggatggcc ccgcaaagcc agcaacaatg ccggagtgtc 540
 gacactgctt gtgatattcc tccccataa agcttg 576

<210> 3
 <211> 401
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:streptavidin
 cDNA (Streptavidin/pUC19)

<220>
 <221> CDS
 <222> (11)..(400)
 <223> streptavidin (Streptavidin/pUC19)

<400> 3
 gaattcgcac atggctgaag ctggtatcac cgggtacttg tacaaccagc tgggggtctac 60
 cttcatcggt accgctggtg ctgacgggtg actgaccggg acttacgaaa gcgctgttgg 120
 taacgctgaa agccgttatg ttctgaccgg tcgttacgac tctgtctcgg ctaccgacgg 180
 ttctggtact gctctgggtt ggaccgttgc ttggaaaaac aactaccgta acgctcactc 240
 tgctaccacc tggctctggcc agtacgttgg tgggtgctgaa gctcgtatca acaccagtg 300
 gctgctgacc tctggtacca ccgaagctaa cgcttggaat tctaccctgg ttggtcacga 360
 cacgttcacc aaagttaaac cgtctgctgc ttctatctag a 401

<210> 4
 <211> 584
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:potato
 proteinase inhibitor II (PPI-II/pUC19)

<220>
 <221> CDS
 <222> (1)..(584)
 <223> PPI-II/pUC19

<220>
 <221> sig_peptide
 <222> (1)..(212)
 <223> signal sequence

<400> 4
 atggatgttc acaaggaagt taatttcggt gcttacctac taattgttct tggtaagatt 60
 ttcctttact cctttgtttt aaaaaataaa aaaacaaaaa aaatccttgg ttatacatat 120
 atatacacac aagtagtttt atttttttcc tttatattat atttggtgta ggaatatttc 180
 tacttggttag cgtggtggaa catggtgatg cgaagatctg tactaaagaa tgtggtaatc 240
 ttgggtttgg gatatgccca cgttcagaag gaagtccgaa aaatcccata tgcatacaatt 300
 gttgctcagg ctataagggt tgtaattatt atagtgtttt cgggagattt atttgcgaa 360
 gagaatctga cctaaaaaac ccaaaagctt gccccctaaa ttgtgatata aatattgcct 420
 attcaagatg cccccattca gaaggaaaat cgctaattta tcccaccgga tgtaccacat 480
 gttgcacagg gtacaagggt tgctactatt tcggtaaaaa tggcaagttt gtatgcgaag 540
 gagagagtga tgaacccaag gcaaatatgt accctgcaat gtga 584

<210> 5
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:altered Bam H I
 site

<400> 5
 ggagatccaa ccatg 15

<210> 6
 <211> 486
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PPI-I/Avidin
 gene fusion

<220>
 <221> CDS
 <222> (1)..(486)
 <223> PPI-I/Avidin fusion protein

<400> 6
 atggagtcaa agtttgctca catcattggt ttctttcttc ttgcaactcc ctttgaaact 60
 ctcttggcac gaaaagaaag tgatggacca gagatccctg ccagaaagtg ctcgctgact 120
 gggaaatgga ccaacgatct gggctccaac atgaccatcg gggctgtgaa cagcagaggt 180
 gaattcacag gcacctacat cacagccgta acagccacat caaatgagat caaagagtca 240
 ccattgcatg ggacacaaaa caccatcaac aagaggaccc agcccacctt tggcttcacc 300
 gtcaattgga agttttcaga gtccaccact gtcttcacgg gccagtgtct catagacagg 360
 aatgggaagg aggtcctgaa gaccatgtgg ctgctgcggt caagtgttaa tgacattggt 420
 gatgactgga aagctaccag ggctcggcatc aacatcttca ctgcctgcg cacacagaag 480
 gactga 486

<210> 7
 <211> 161
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PPI-I/Avidin
 fusion protein

<400> 7

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Met Glu Ser Lys Phe Ala His Ile Ile Val Phe Phe Leu Leu Ala Thr
 1           5           10           15
Pro Phe Glu Thr Leu Leu Ala Arg Lys Glu Ser Asp Gly Pro Glu Ile
          20           25           30
Pro Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr Asn Asp Leu Gly
          35           40           45
Ser Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly Glu Phe Thr Gly
          50           55           60
Thr Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu Ile Lys Glu Ser
          65           70           75           80
Pro Leu His Gly Thr Gln Asn Thr Ile Asn Lys Arg Thr Gln Pro Thr
          85           90           95
Phe Gly Phe Thr Val Asn Trp Lys Phe Ser Glu Ser Thr Thr Val Phe
          100          105          110
Thr Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys Glu Val Leu Lys Thr
          115          120          125
Met Trp Leu Leu Arg Ser Ser Val Asn Asp Ile Gly Asp Asp Trp Lys
          130          135          140
Ala Thr Arg Val Gly Ile Asn Ile Phe Thr Arg Leu Arg Thr Gln Lys
          145          150          155          160
Glu

```

<210> 8
 <211> 626
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial
 Sequence:PPI-II/Streptavidin gene fusion

<220>

<221> CDS

<222> (1)..(626)

<223> PPI-II/Streptavidin fusion protein

<220>

<221> modified_base

<222> (585)

<223> n = g, a, c or t

<400> 8

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atgggatgttc acaaggaagt taatttcggt gcttacctac taattgttct tggttaagatt 60
ttcctttact cctttgtttt aaaaaataaa aaaacaaaaa aaatcttggt ttatacatat 120
atatacacac aagtagtttt atttttttcc tttatattat atttggtgta ggaatatttc 180
tacttgtagt cgtggtggaa catggtgatg cgaagatctg tactaagaat tcgcatatgg 240
ctgaagctgg tatcaccggt acttggtaca accagctggg gtctaccttc atcgttaccg 300
ctggtgctga cgggtgactg accggtactt accgaaagcgc tgttggtaac gctgaaagcc 360
gttatgttct gaccggtcgt tacgaactctg ctccggctac cgacggttct ggtactgctc 420
tggtgttgac cggtgcttgg aaaaacaact accgtaacgc tcactctgct accacctggt 480

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ctggccagta cgttggtggt gctgaagctc gtatcaacac ccagtggctg ctgacctctg 540
gtaccaccga agctaacgct tggaaatcta ccctggttgg tcacnacacg ttcaccaaag 600
ttaaaccgtc tgctgcttct atctag                                     626

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<210> 9
<211> 168
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial
      Sequence:PPI-II/Streptavidin fusion protein

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```

<400> 9
Met Asp Val His Lys Glu Val Asn Phe Val Ala Tyr Leu Leu Ile Val
  1           5           10          15
Leu Gly Ile Phe Leu Leu Val Ser Val Val Glu His Val Asp Ala Lys
      20           25           30
Ile Cys Thr Lys Asn Ser His Met Ala Glu Ala Gly Ile Thr Gly Thr
      35           40           45
Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala Asp
      50           55           60
Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser
      65           70           75           80
Arg Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly
      85           90           95
Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg
      100          105          110
Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala
      115          120          125
Glu Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu
      130          135          140
Ala Asn Ala Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr Lys
      145          150          155          160
Val Lys Pro Ser Ala Ala Ser Ile
      165

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<210> 10
<211> 638
<212> DNA
<213> Streptomyces avidinii

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<220>
<221> CDS
<222> (50)..(601)
<223> streptavidin

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<220>
<221> sig_peptide
<222> (50)..(121)
<223> signal sequence

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<400> 10
ccctccgtcc ccgccgggca acaactaggg agtatttttc gtgtctcac atg cgc aag 58
Met Arg Lys
1

```

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atc gtc gtt gca gcc atc gcc gtt tcc ctg acc acg gtc tcg att acg 106
Ile Val Val Ala Ala Ile Ala Val Ser Leu Thr Thr Val Ser Ile Thr
      5              10              15

gcc agc gct tcg gca gac ccc tcc aag gac tcg aag gcc cag gtc tcg 154
Ala Ser Ala Ser Ala Asp Pro Ser Lys Asp Ser Lys Ala Gln Val Ser
      20              25              30              35

gcc gcc gag gcc ggc atc acc ggc acc tgg tac aac cag ctc ggc tcg 202
Ala Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly Ser
              40              45              50

acc ttc atc gtg acc gcg ggc gcc gac ggc gcc ctg acc gga acc tac 250
Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr Tyr
              55              60              65

gag tcg gcc gtc ggc aac gcc gag agc cgc tac gtc ctg acc ggt cgt 298
Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly Arg
              70              75              80

tac gac agc gcc ccg gcc acc gac ggc agc ggc acc gcc ctc ggt tgg 346
Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly Trp
      85              90              95

acg gtg gcc tgg aag aat aac tac cgc aac gcc cac tcc gcg acc acg 394
Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser Ala Thr Thr
      100              105              110              115

tgg agc ggc cag tac gtc ggc ggc gcc gag gcg agg atc aac acc cag 442
Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile Asn Thr Gln
              120              125              130

tgg ctg ctg acc tcc ggc acc acc gag gcc aac gcc tgg aag tcc acg 490
Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser Thr
              135              140              145

ctg gtc ggc cac gac acc ttc acc aag gtg aag ccg tcc gcc gcc tcc 538
Leu Val Gly His Asp Thr Phe Thr Lys Val Lys Pro Ser Ala Ala Ser
              150              155              160

atc gac gcg gcg aag aag gcc ggc gtc aac aac ggc aac ccg ctc gac 586
Ile Asp Ala Ala Lys Lys Ala Gly Val Asn Asn Gly Asn Pro Leu Asp
      165              170              175

gcc gtt cag cag tag tcgcgtcccgcgaccggcggtgcccgggacctcggcc 638
Ala Val Gln Gln
180

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<210> 11
<211> 183
<212> PRT
<213> Streptomyces avidinii

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<400> 11
Met Arg Lys Ile Val Val Ala Ala Ile Ala Val Ser Leu Thr Thr Val
      1              5              10              15
Ser Ile Thr Ala Ser Ala Ser Ala Asp Pro Ser Lys Asp Ser Lys Ala
              20              25              30
Gln Val Ser Ala Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln
      35              40              45

```

Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr
 50 55 60
 Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu
 65 70 75 80
 Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala
 85 90 95
 Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser
 100 105 110
 Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile
 115 120 125
 Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp
 130 135 140
 Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr Lys Val Lys Pro Ser
 145 150 155 160
 Ala Ala Ser Ile Asp Ala Ala Lys Lys Ala Gly Val Asn Asn Gly Asn
 165 170 175
 Pro Leu Asp Ala Val Gln Gln
 180

<210> 12
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:forward M13
 (lacZ) primer [Perkin Elmer]

<400> 12
 gccagggttt tcccagtcac ga

22

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:reverse M13
 (lacZ) primer [Perkin Elmer]

<400> 13
 gagcggataa caatttcaca cagg

24

<210> 14
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:avidin upstream
 primer

<400> 14
 gcacacccgg ctgtccacct g

21

<210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PPI-I
 phosphorylated mutagenic primer

<220>
 <221> modified_base
 <222> (1)
 <223> n = 5' phosphorylated g

<400> 15
 natggaccag agatcttaga ac

22

<210> 16
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:avidin
 phosphorylated mutagenic primer

<220>
 <221> modified_base
 <222> (1)
 <223> n = 5' phosphorylated g

<400> 16
 ngctcccggg atccctgcca g

21

<210> 17
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR sense
 primer

<400> 17
 ctgcaggtcg actctagagg a

21

<210> 18
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR antisense
 primer

<400> 18
 ggtgaattct tagtacagat ottcgca

27